Preliminary studies on microarray analysis of gene expression during cold acclimation in blueberry

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To monitor changes in gene expression associated with cold acclimation in the woody perennial blueberry (*Vaccinium* spp.), a genomics approach base on cDNA microarrays was undertaken using ~2400 ESTs generated from 2 cDNA libraries that were constructed using RNA isolated from cold acclimated floral buds (collected in mid winter conditions) and non-acclimated floral buds (collected in fall). cDNA inserts were amplified from the plasmids, purified and arrayed onto glass slides. RNA was isolated from floral buds collected from field grown plants of the relatively cold hardy cultivar 'Bluecrop' that received 0, 70, 400, 800 and 1200 chill hours and from greenhouse/cold room-grown plants that received 0, 500, and 1000 chill hours. Total RNA was used to make cDNAs, which were labeled with Alexa Flour 555 and Alexa Flour 647 dyes. Dye-swap labeling was carried out on two biological replicates. After hybridization, slides were scanned, data normalized using lowess print-tip method and ratios of the two signals estimated to determine relative levels of transcripts after different exposures to low temperature. T-tests and ANOVA will be used to determine statistically significant up and down-regulated genes with cold acclimation under field and cold room conditions.